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84  ySAspAsnGlyThrThrThrAlaSerGluAsnHisLeuThrGlnCysLeu 100
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117  sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgL 134
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368  ATATTGGAGTGAAGAAATTTTCAGTGTCTTCAATGAAAGTAAAGTCTGCTC 417
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seq_name: SwissProt_39:TNF1_MOUSE
seq_documentation_block:
AC P25118; STANDARD; PRT; 454 AA.
DI 01-MAY-1992 (Rel. 22, Created)
DI 01-MAY-1992 (Rel. 22, Last sequence update)
DI 20-APR-2001 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 P60 (TNF-P1) (TNF-P1)
DE (P55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
PN [1]
RN
SEQUENCE FROM N.A.
RX MEDLINE-91187885; PubMed-1819278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA Wong G.H., Chen E.Y., Goeddel D.V.
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific."
RI Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RN
SEQUENCE FROM N.A.
RX MEDLINE-91246168; PubMed-1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith G.A.
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor."

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FN [3]
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SEQUENCE FROM N.A.
RX MEDLINE-91285014; PubMed-1647956;
RA Barrett K., Taylor Fishwick D.A., Cope A.P., Kissenerqhis A.M.,
RA Gray P.W., Feldmann M., Foxwell B.M.J.
RT "Cloning, expression and cross-linking analysis of the murine p55
RT tumor necrosis factor receptor."
RI Eur. J. Immunol. 21:1649-1656(1991).
RN [4]
RN
SEQUENCE FROM N.A.
RX TISSUE-Spleen;
RX MEDLINE-92039815; PubMed-1657766;
RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.
RT "Molecular cloning and expression of the mouse Tnf receptor type b."
RN [5]
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SEQUENCE FROM N.A.
RX MEDLINE-91245292; PubMed-8188124;
RA Robo B.P., Lenthicum D.S.
RT "Nucleotide sequence of the TNF type I receptor from a mouse
RT endothelioma cell line."
RI Immunogenetics 39:450-451(1994).
RN [6]
RN
SEQUENCE FROM N.A.
RX MEDLINE-93156721; PubMed-8381516;
RA Rothe T., Blumberg P., Gentz R., Lesslauer W., Steiertz M.
RT "Genomic organization and promoter function of the murine tumor
RT necrosis factor receptor beta gene."
RI Mol. Immunol. 30:165-175(1993).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC ASSEMBLY CALLED THE DEATH INDUCING SIGNALING COMPLEX (DISC)
CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC -1- SUBUNIT: INF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGRP/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
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CC entities requires a license agreement (see http://www.isb.sib.ch/annouce/
CC or send an email to license@sib.sib.ch).
CC
CC EMBL: M60468; AAA39751.1; -
CC EMBL: M59377; AAA40464.1; -
CC EMBL: X59238; CAA41922.1; -
CC EMBL: X57796; CAA40936.1; -
CC EMBL: I26449; AAA59461.1; -
CC EMBL: M76656; AAA40465.1; -
CC EMBL: M88067; AAA40465.1; JOINED.
CC EMBL: M76655; AAA40465.1; JOINED.
CC PIR: A38634; GQMST1.
CC PIR: S16677; S16677.
CC PIR: S19021; S19021.
CC HSSP: P19438; 1EXT.
CC MGD: MGI:1314884; Tnfrs1a.
CC InterPro: IPR000488; Death.
CC InterPro: IPR001368; TNFR_c6.
CC Pfam: PF00531; death_1.
CC Pfam: PF00020; TNFR_c6; 4.

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EMBL: M63122; AAA12256.1; -.
PIR: B36555; B36555.
HSSP: P19448; TNF.
InterPro: IPR000488; Death.
InterPro: IPR001368; TNF_c6.
Pfam: PF00541; death; 1.
Pfam: PF00020; TNF_c6; 4.
ProDom: PD000771; TNF_c6; 1.
SMART: SM00005; DEATH; 1.
SMART: SM00208; TNF; 3.
SMART: SM00652; TNF_NGFR_1; 3.
PROSITE: PS00050; TNF_NGFR_2; 3.
PROSITE: PS00017; DEATH_DOMAIN; 1.
KW Receptor, Transmembrane, Glycoprotein, Repeat, Signal, Apoptosis.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 461 TMOR NECROSIS FACTOR RECEPTOR 1.
FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 231 POTENTIAL.
FT DOMAIN 235 461 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 43 196 4 X TNF-CYS.
FT REPEAT 43 82 TNF-CYS 1.
FT REPEAT 84 125 TNF-CYS 2.
FT REPEAT 126 166 TNF-CYS 3.
FT REPEAT 167 196 TNF-CYS 4.
FT DOMAIN 344 354 N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 363 448 DEATH.
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FT DISULFID 62 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
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FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 174 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 185 195 BY SIMILARITY.
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FT CARBOHYD 151 151 N-LINKED (GLNAC) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLNAC) (POTENTIAL).
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alignment_scores:

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Ratio: 4.583 Gaps: 1
Percent Similarity: 80.476 Percent Identity: 64.762

alignment_block:

US-09-525-998a-11 x TNF1_PAT

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268 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 317
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ID TNF1_BOVIN STANDARD; PRT; 471 AA.
AC 019131.
DT 26-AUG-2001 (rel. 40, Created)
DT 20-AUG-2001 (rel. 40, Last sequence update)
DT 20-AUG-2001 (rel. 40, Last annotation update)
FE 13MOR NECROSIS FACTOR RECEPTOR 1 HOMOLOGY (P55) (P55)
DE (P55).
GN TNFRSF1A OR TNF1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Korta;
RA Lee E.-K., Talyor M.J., Kehrli M.E.;
RT "Cloning of cDNA encoding bovine tumor necrosis factor receptor 1
(RTNFR-1).";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC AGGREGATE CALLED THE DEATH INDUCING SIGNALING COMPLEX (DISC)
CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED, THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND

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RT "A lymphotoxin-beta-specific receptor.";
 RL Science 264:707-713(1994).
 CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
 CC IMMUNE DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NFPP/TNFR-TYPE CYSTEINE-RICH REGION.
 CC
 CC This SWISS-PROT entry is obsolete. It is replaced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
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EMBL: U04270; AAA36757.1; -;
 DDB: U04270; AAA36757.1; -;
 DR HMM: 600979; -;
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR ProDom: PD000977; TNFR_c6; 1.
 DR SMART: SM00208; TNFR_4.
 DR PROSITE: PS00652; TNFR_NFPP_1; 2.
 DR PROSITE: PS00650; TNFR_NFPP_2; 3.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 435 LYMPHOTOXIN-BETA RECEPTOR.
 FT DOMAIN 228 248 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 249 445 POTENTIAL.
 FT DOMAIN 42 211 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 42 211 4 X TNFR-CYS.
 FT REPEAT 42 81 TNFR-CYS 1.
 FT REPEAT 82 124 TNFR-CYS 2.
 FT REPEAT 125 168 TNFR-CYS 3.
 FT REPEAT 169 211 TNFR-CYS 4.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 80 BY SIMILARITY.
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 FT DISULFID 104 124 BY SIMILARITY.
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 Percent Similarity: 51.869 Percent Identity: 30.841

alignment_block:

US-09-525-998a-11 x INRC_HUMAN

Align seq 1/1 to: TNRC_HUMAN from: 1 to: 435

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 22 LeuAlaAlaSerGlnProGlnAlaValProGlyValAlaSer 38
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 39 GluAsnGlnThrCysArgAspGlnGlnGlySerGlyTrpCysArgGln 55
 129 TAAATCGATTGCTGTACCAAGTGCACAAAGAACCTACTTCTGTAATATG 178

55 SAIRG...IleCysCysSerAlaCysProGlyIleTrpValSerAlaL 71
 179 ACTGTCCAGGCCCGGCGGACATACGACATCCAGGAGTGTGAGAGCGGC 228
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 AC Q99830;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 40, Last annotation update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
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 DE MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN)
 DE (APOPTOSIS INDUCING RECEPTOR AIR) (APO-4) (LYMPHOCYTE ASSOCIATED
 DE RECEPTOR OF DEATH) (IARD).
 GN TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SOURCE FROM N.A.; ALTERNATIVE SPLICING, AND MUTAGENESIS.
 RC TISSUE=Lymphoid;
 RX MEDLINE=97088617; PubMed=8934525;
 RA Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pan K.-T.,
 RA Griffin C.J., Brown K., Fallow S.N.;
 RT "A death domain-containing receptor that mediates apoptosis.";
 RL Nature 384:372-375(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Umbilical vein endothelial cells;
 RX MEDLINE=97081063; PubMed=8875942;
 RA Chinnaiyan A.M., O'Rourke K., Yu G.-I., Lyons R.H., Garg M.,
 RA Hudson B.K., Xing L., Gentry R., Ni J., Dixit V.M.,
 RT "Signal transduction by DR3, a death domain-containing receptor
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212 LysHisSerLeuValThrCysThrSerSerSerSerSerSerSer 227

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seq_documentation_block:

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ID TNR2_MOUSE STANDARD; PRT; 474 AA.
AC P25119; P47891;
DT 01-MAY-1992 (rel. 22, Created)
DT 15-MAY-1999 (rel. 48, Last sequence update)
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GN TNFRSF10 OR TNFR2 OR TNFR 2.
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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RX MEDLINE=9118785; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific."
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991)
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson P., Jerzy P., Davis T., Brannan C.L.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor."
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [4]
RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=NOB;
RA Jacob C.O., Liu J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/TrnB databases
RN [4]

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RP TISSUE=Liver;
RA Kissinger M., Fellous R., Feldman M., Chertajovsky Y.;
RL Submitted (MAY-1995) to the EMBL/GenBank/TrnB databases
CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA
CC -!- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NSEP/INP-1/YPE CYSTEINE-PATH REGION
CC
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CC

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DR EMBL: M60469; AAA34752.1;
DR EMBL: M59378; AAA0463.1;
DR EMBL: U39488; AAA85021.1;
DR EMBL: X87128; CAA60618.1;
DR PIR: R38634; R38634
DR HSSP: P19438; INCF;
DR MGD: MGI:131488; tnfrsf1b;
DR InterPro: IPR001368; TNFR_c6;
DR Pfam: PF00329; TNFR_c6; 4

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DP ProDom: PD000771; TNFR_c6; 1.
DR SMPT: SM00208; TNFR_4;
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00050; TNFR_NGFR_2; 3.
KW Receptor, Transmembrane, Glycoprotein, Repeat, Signal.
FT SIGNAL 1 22
FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2
FT DMAIN 23 258 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 259 288 POTENTIAL.
FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 203 4 X TNFR-CYS.
FT REPEAT 39 77 TNFR-CYS 1.
FT REPEAT 78 119 TNFR-CYS 2.
FT REPEAT 120 164 TNFR-CYS 3.
FT REPEAT 165 203 TNFR-CYS 4.
FT DISULFID 40 54 HY SIMILARITY.
FT DISULFID 55 68 HY SIMILARITY.
FT DISULFID 58 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 149 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 89 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 474 AA; 50319 MW; 4521AF496C406564 CPCb4;

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alignment_scores: Quality: 181.00 Length: 161
Ratio: 1.946 Gaps: 8
Percent Similarity: 57.764 Percent Identity: 31.677

alignment_block:

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Align seq 1/1 to: TNR2_MOUSE from: 1 to: 474
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111 111111 111111 111111 111111 111111
40 CysGlnIleSerGlnGluTyrTyrAspArgLysAlaGlnMetCysCysAl 56
147 CAAGTGGCCACAAAGCAAGCTACTGTCACAAACGCTGCGACGCGCGGCGC 196
111111 111111 111111 111111 111111
56 GlySerProProGlyGlyGlyValIlyshisPheCys...AsnLysThr: S 72
197 AGATATAGGATTCAGAGAGATGATGAGAGAGATGATGATGATGATGATG 246
111111 111111 111111 111111 111111
72 GlAspThrValCysAlaAspCysGluAlaSerMotIyThrGlnValTrp 88
247 AATGATCTTACACACACACACACACACACACACACACACACACACACAC 293
111111 111111 111111 111111 111111
69 AsnIlePheArgThrCysLeuSerCysSerSerSerSerSerSerThrAsp 104
294 GCGTCAGTGGACAGTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 343
111111 111111 111111 111111 111111
105 GlnValGlnIleArgAlaCysThrIlyshisPheCysAlaGlnValCysAl 120
344 GTCGTAGCAAAACATGATG 381
111 111111 111111 111111 111111
120 LaCysGluAlaClyArgIlyCysAlaIleulysThrHis.....SerCly 134
382 AATGCTTTTCCAGTGGACACATGATGATGATGATGATGATGATGATGAT 428
111 111111 111111 111111 111111
135 SerCysArgGlnCysMetArgLeuSerCysCysIlyProGlyPheGlyVa 151
429 GCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 475
111 111111 111111 111111 111111
151 AlaSerSerArgAlaProGlnGlyAsnValIleCysCysAlaCysAlap 168
476 CAGGTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 525

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